```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM nucleic - nucleic search, using sw model

Run on:

February 18, 2003, 09:20:45 ; Search time 48 Seconds
(without alignments)
5513.793 Million cell updates/sec

us-10-021-811-35 863 Title: Perfect score: Sequence:

OLIGO_NUC Gapop 60.0 , Gapext 60.0 Scoring table:

441362 seqs, 153338381 residues Searched:

9

Word size :

0 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodatex1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodatex1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodatex1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodatex1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodatex1/ina/PcTUS_COMB.seq:*
6: /cgn2_6/ptodatex1/ina/PcTUS_COMB.seq:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Π Query Score Match Length DB Result

Description

No matches found

Search completed: February 18, 2003, 10:32:30 Job time : 48 secs

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Gaps 9 9

ö

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Length 863; Indels 240

240

300 360 420

540

540

780

480

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CCCTACAATTAATCCTGATCAATCCAGTTGTTGTACCAATGACAACAACAACAATTAACTA 600
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                                                                                                                                                                                                                                                        TATTGCAAATCATGGGGAAGGTGTTTGGAACTCTTTGGCCAAAGCTGCTGGTCTCAAACG 180
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                                                                                                                                                                                                                                                                                                                                                    TAACGGAAAGAGTTGCCGGCTAAGGTGGCTAAATTACCTCCGTCCTGATGTTAGAAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                 241 GAATATTACACCCGAGGAACAACTTTTGATTATGGAGCTCCACGCAAAGTGGGGAAACAG
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Pred. No. 4.6e-301;
                                                                                                                                                            0; Mismatches
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Microsoft Office 97
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAAAAAAAAAAAAAAAAA 863
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100.0%;
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                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 863; Conservative
                                                              ; LENGTH: 863
; TYPE: DNA
; ORGANISM: Glycine max
US-10-021-811-35
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                                                                                                       (without alignments)
7449.937 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                        Search time 59 Seconds
                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/pubpna/US10_pUBCOMB.seq:*/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /ptodata/1/pubpna/US10_NEW_PUB.seg:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31, Application US/10021811
Publication No. US20030024007A1
GENERAL INFORMATION.
GENERAL INFORMATION.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Odell, Joan
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
FILE REFERENCE: B81294 US NA
CURRENT APPLICANT NUMBER: US/10/021,811
CURRENT FILING DATE: 2001-12-14
            5.1.3
Compugen Ltd.
                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            863 9 US-10-021-811-35
                                                                                                                                                                                                                                       424239 segs, 254661826 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
            version - 2003
                                                                                         February 18, 2003, 09:21:50
                                                                                                                                                                                                                                                                                                                                                              Post-processing: Listing first 45 summaries
                                                              nucleic search, using sw model
                                                                                                                                                                                                             Gapop 60.0 , Gapext 60.0
            GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                    length: 0
length: 2000000000
                                                                                                                                           US-10-021-811-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/
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                                                                                                                                                                                                                                                                                                                     Minimum DB seq
Maximum DB seq
                                                                                                                                                          Perfect score:
                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                  Word size :
                                                              OM nucleic
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9
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Description

Π

SUMMARIES

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                           Search completed: February 18, 2003, 10:02:37 Job time : 2196 secs
                                                    Query
Score Match Length DB
                                                                                             No matches found
                                                                     February 18, 2003, 08:51:00 ; Search time 2196 Seconds
(without alignments)
11437.032 Million cell updates/sec
                                                                                                                                       Pred. No. is the number of results predicted by chance to have a
         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                       0
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                                                                                                                                                                                         2054640 segs, 14551402878 residues
                                                                                                                                                                                                                                                                                         Post-processing: Listing first 45 summaries
                                                 OM nucleic - nucleic search, using sw model
                                                                                                                                                    Gapop 60.0 , Gapext 60.0
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em_htgo_hum:*
em_htgo_mus:*
em_htgo_other:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_un:*
em_vi:*
em_htg_hum:*
em_htg_inv:*
em_htg_other:*
em_htg_mus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_htg_rod:*
em_htg_rod:*
em_htg_mam:*
em_htg_wrt:*
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Maximum DB seq length: 200000000
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863
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9b_ph:*
9b_pl:*
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9b_pr:*
9b_yes:*
9b_sts:*
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em_ln:*
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Perfect score:
Sequence:
                                                                                                                                                          Scoring table:
                                                                                                                                                                                                              Word size :
                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                           Searched:
                                                                        Run on:
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February 18, 2003, 08:14:20 ; Search time 220 Seconds (without alignments) 8833.975 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | SIDS2/gcgdata/geneseqremenb_/NA1981.pdf:*
| SIDS2/gcgdata/geneseqremenb_/NA1984.DaT:*
| SIDS2/gcgdata/geneseqremenb_/NA1984.DaT:*
| SIDS2/gcgdata/geneseqremenb_/NA1984.DaT:*
| SIDS2/gcgdata/geneseqremenb_/NA1986.DaT:*
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| SIDS2/gcgdata/geneseqremenb_/NA1997.DaT:*
| SIDS2/gcgdata/geneseqremenb_/NA20018.DaT:*
| SIDS2/gcgdata/geneseqremenb_/NA20018.DaT:*
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| SIDS2/gcgdata/geneseqremenb_/NA20018.DaT:*
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                                                                                                                                                                                                                                                                                                                                                                                                    N_Geneseq_101002:*
... /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
.: /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
.: /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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863
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115.:
117.:
119.:
220.:
221.:
24.:
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Sequence:
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                                                                                                                                                                                                    Run on:
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Description

f

Query Match Length DB

Score

Result No.

SUMMARIES

Search completed: February 18, 2003, 09:25:40 Job time: 221 secs

No matches found

9

DEFINITION

RESULT 8 CPU33917

a

ACCESSION

KEYWORDS

ORGANISM

REFERENCE AUTHORS

TITLE

```
/trail it ion-"MDEKGRSLKNNNMEDEMDLKRCPWTAEEDFKLMNY IATNCECRW
NSLSRCAGLQRTGKSCRLRMLNYLRPDVRRGNITLEEQLLILELHSRWGNRWSKIAQY
LPGRYDNETKNYRMTRYOVHARQLKCDVNSQORDPKTLDMPRLYDERLOGASASAA
AATTTTTTTTGSTSCITTSNNOFMY DY NNNMGOQFCWASNNDY ITPENSSAS
SPASDLTEYSANDRPRY XSQQMGNSY YPQONLYSSQCLLDDNY PSYSGLLDEDLTAM
OEGSNLSWFENINGAASSSDSLWNIGETDEEFWFLQQQQQFNNNGSF"
                                                                                                                                                                                                                                                                                                                                                                   AF262733 1423 bp mRNA linear PLN 30-AUG-2001
Arabidopsis thaliana putative transcription factor MYB108 (MYB108)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
Eukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta;
Spermatophyta: Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1423)
Stracke, R., Werber, M. and Weisshaar, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-MAY-2000) Biochemie, Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln D-50829, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 (bases 1 to 1423)
Stracke, R. and Weisshaar, B.
Direct Submission
Submitted (29-AUG-2010)
Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg
10, Koeln D-50829, Germany
Sequence update by submitter
On Aug 30, 2001 this sequence version replaced gi:8101955.
Location/Qualifiers
244 TATTACACCCGAGGAACATTTTGATTATGGAGCTCCACGCAAAGTGGGGGAAACAGGG 303
                                                                                               304 GTCCAAAATTGCCAAGCATCTACCTGGAAGGACTGATAATGAGATCAAGAACTATTGGAG 363
                                                                                                                            373 TATCACACTCGAAGAACAGCTTCTCATTCTTGAACTCCATTCTCGTTGGGGCAATAGGTG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"At3g06490; member of the R2R3-MYB family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative transcription factor MYB108" /protein_id="AAF72668.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /hote="alternative transcription start site"
155. :1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The R2R3-WYB gene family in Arabidopsis thaliana Curr. Opin. Plant Biol. 4 (5), 447-456 (2001) 21481677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .1423 /
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="ecotype: Columbia"
                                                                                                                                                                                                                         493 AACGAGGGTCCAAAAACATGCCAAACA 519
                                                                                                                                                                                                 364 GACAAGGATCCAGAAGCACATCAAGCA 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 1423)
Stracke, R. and Weisshaar, B.
Direct Submission
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5
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                                                                                                                                    Craterostigma plantagineum myb-related transcription factor (cpm7) mRNA, complete cds. 033917.1 GI:1002799
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/note="putative DNA-binding protein; Description: myb-like
gene; myb-related transcription factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSK IAQHLPGRTDNEI KNYWRTRVQKHAKQLKCDVNSKQFKDTMRYLWRPLVERIQR
AATUDDAAPPLASSASESAMMYACYSTAMAAGDHRRQFKIMDQYYYAWTHSNIMIA
QENSSTVASSESTECSI.SSELTEMYA ANYHQYI NGADHQQIDSSTTTSYGWQNDPAINY
VGNNGNSDQLGMGSVDDRRSNEQWAMADDVDNGGSSDKDNNLLWNVDDVWFLQQPSSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A family of novel myb-related genes from the resurrection plant craterostidyma plantagineum are specifically expressed in callus and roots in response to ABA or desiccation
Plant Mol. Biol. 32 (4), 707-716 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MNQQQVVKVSKNKQINSEDDDDSSDLRRGPWTVDEDFTLINYIA
HHGEGRWNSLARFAGLKRTGKSCRLRWLNYLRPDVRRGNITLEEQLLILELHSRWGNR
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                                                                                                                                                                                                                                                                                                                Craterostigma plantagineum Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Lamiales; Lamiales incertae sedis; Torenieae; Craterostigma. I Lamana I to 1295) I thases I to 1295) Ituriaga G., Leyns, L., Villegas, A., Gharalbeh, R., Salamini, F. and Bartels, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (14-AUG-1995) Gabriel Iturriaga, Plant Molecular Biology,
Instituto de Biotecnología, Av. Universidad #2001, Cuernavaca, MOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 TGCAAATCATGGGGAAGGTGTTTGGAACTCTTTGGCCAAAGCTGCTGGTCTCAAACGTAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 CGGAAAGAGTTGCCGGCTAAGGTGGCTAAATTACCTCCGTCCTGATGTTAGAAGAGGGAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 TCCTGAAGTGAGAAAAGGGCCTTGGACAATGGAAGAAGACTTGATCTTGATGAACTATAT 123
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/db_xref="taxon:4153"
1. 1295
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Pred. No. 9.1e-28;
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/db_xref="G1:1002800"
                       450 AACAAGGGTCCAAAAACATGCCAAACA 476
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125. .1132
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Matches 232; Conservative
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Nirect Submission
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